

## WEST Search History

DATE: Tuesday, February 21, 2006

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L1	(Pmepa1 or pmepa-1 or mivr1 or mivr-1) same (gene or sequence or \$1dna or protein or \$5peptide)	16

END OF SEARCH HISTORY



# results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1140558082-32062-97435568291.BLASTQ4

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
3,743,317 sequences; 16,630,950,921 total letters

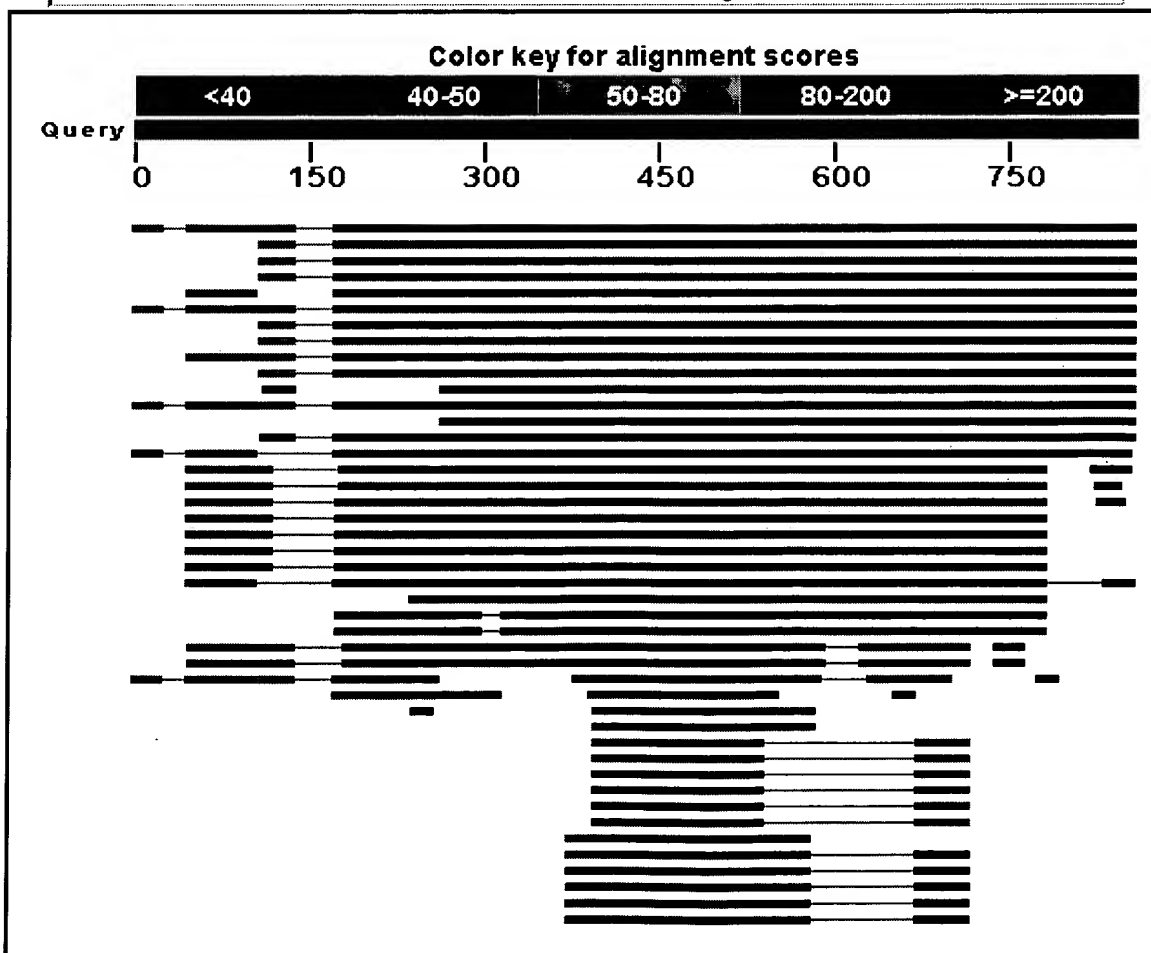
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

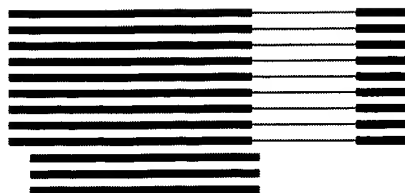
**Query=**

Length=861

## Distribution of 140 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments





Sequences producing significant alignments:				Score (Bits)	E Value
gi 40317614 ref NM_020182.3	Homo sapiens transmembrane, pros...	1322	0.0		
gi 40317615 ref NM_199169.1	Homo sapiens transmembrane, pros...	1322	0.0		
gi 40317619 ref NM_199171.1	Homo sapiens transmembrane, pros...	1322	0.0		
gi 40317617 ref NM_199170.1	Homo sapiens transmembrane, pros...	1322	0.0		
gi 50492890 emb CR612083.1	full-length cDNA clone CS0DJ015YF...	1322	0.0		
gi 16303741 gb AF305616.1 AF305616	Homo sapiens STAG1/PMEPA1 mRNA	1322	0.0		
gi 22121998 gb AY128643.1	Homo sapiens PMEPA1 variant A protein	1322	0.0		
gi 9255808 gb AF224278.1 AF224278	Homo sapiens PMEPA1 protein (P	1322	0.0		
gi 16198474 gb BC015918.1	Homo sapiens transmembrane, prosta...	1314	0.0		
gi 51593770 gb BC080635.1	Homo sapiens transmembrane, prosta...	1298	0.0		
gi 11546043 emb AL035541.15 HS718J7	Human DNA sequence from c...	1039	0.0		
gi 15824468 gb AF305426.1 AF305426	Homo sapiens solid tumor-a...	1039	0.0		
gi 55652999 ref XM_514746.1	PREDICTED: Pan troglodytes LOC45836	995	0.0		
gi 73992626 ref XM_543070.2	PREDICTED: Canis familiaris simi...	872	0.0		
gi 82524234 emb CR956367.12	Pig DNA sequence from clone PigE...	644	0.0		
gi 18605637 gb BC023092.1	Mus musculus cDNA clone IMAGE:3989996	531	1e-147		
gi 23331176 gb BC036995.1	Mus musculus transmembrane, prosta...	531	1e-147		
gi 12843488 dbj AK008976.1	Mus musculus adult male stomach c...	529	5e-147		
gi 62027429 gb BC092094.1	Mus musculus cDNA clone IMAGE:3153171	529	5e-147		
gi 47124388 gb BC069890.1	Mus musculus transmembrane, prosta...	529	5e-147		
gi 31340603 ref NM_022995.2	Mus musculus transmembrane, pros...	529	5e-147		
gi 74201952 dbj AK136450.1	Mus musculus adult male colon cDN...	521	1e-144		
gi 62646459 ref XM_230899.3	PREDICTED: Rattus norvegicus tra...	464	2e-127		
gi 12004973 gb AF220208.1 AF220208	Mus musculus Nedda4 WW doma...	450	3e-123		
gi 82887825 ref XM_913670.1	PREDICTED: Mus musculus similar ...	424	2e-115		
gi 32398588 emb AL837509.11	Mouse DNA sequence from clone RP...	418	1e-113		
gi 53133895 emb AJ720618.1	Gallus gallus mRNA for hypothetical	303	5e-79		
gi 71895608 ref NM_001031492.1	Gallus gallus similar to Tran...	303	5e-79		
gi 7161781 emb AL121913.4 HSJ1059L7	Human DNA sequence from c...	182	1e-42		
gi 73945987 ref XM_541100.2	PREDICTED: Canis familiaris hypo...	178	2e-41		
gi 76651938 ref XM_588908.2	PREDICTED: Bos taurus hypothetical	168	2e-38		
gi 76633111 ref XM_869738.1	PREDICTED: Bos taurus similar to...	163	1e-36		
gi 68384134 ref XM_679680.1	PREDICTED: Danio rerio similar t...	157	7e-35		
gi 31790549 emb BX005347.5	Zebrafish DNA sequence from clone...	157	7e-35		
gi 34556291 gb AC111069.9	Mus musculus chromosome 18, clone ...	137	7e-29		
gi 26342572 dbj AK052338.1	Mus musculus 13 days embryo heart...	137	7e-29		
gi 26333688 dbj AK040289.1	Mus musculus 0 day neonate thymus...	137	7e-29		
gi 18490514 gb BC022716.1	Mus musculus DNA segment, Chr 18, ...	137	7e-29		
gi 31324574 ref NM_172631.2	Mus musculus DNA segment, Chr 18...	137	7e-29		
gi 66272338 gb BC096371.1	Mus musculus DNA segment, Chr 18, ...	137	7e-29		

gi 55647658 ref XM 512194.1	PREDICTED: Pan troglodytes simil...	131	4e-27
gi 22539691 gb BC030199.1	Homo sapiens chromosome 18 open re...	131	4e-27
gi 20455845 gb BC029958.1	Homo sapiens chromosome 18 open re...	131	4e-27
gi 51093709 ref NM 001003675.1	Homo sapiens chromosome 18 op...	131	4e-27
gi 51093707 ref NM 001003674.1	Homo sapiens chromosome 18 op...	131	4e-27
gi 51093712 ref NM 004338.2	Homo sapiens chromosome 18 open ...	131	4e-27
gi 51093722 ref NM 181483.2	Homo sapiens chromosome 18 open ...	131	4e-27
gi 51093715 ref NM 181482.2	Homo sapiens chromosome 18 open ...	131	4e-27
gi 51093725 ref NM 181481.2	Homo sapiens chromosome 18 open ...	131	4e-27
gi 16549670 dbj AK055028.1	Homo sapiens cDNA FLJ30466 fis, c...	131	4e-27
gi 2271474 gb AF009427.1 AF009427	Homo sapiens clone 22 mRNA,...	131	4e-27
gi 2271472 gb AF009426.1 AF009426	Homo sapiens clone 22 mRNA,...	131	4e-27
gi 2271470 gb AF009425.1 AF009425	Homo sapiens clone 22 mRNA,...	131	4e-27
gi 2271468 gb AF009424.1 AF009424	Homo sapiens clone 22 mRNA,...	131	4e-27
gi 21728137 dbj AP001010.4	Homo sapiens genomic DNA, chromos...	131	4e-27
gi 68444170 ref XM 694964.1	PREDICTED: Danio rerio similar t...	123	1e-24
gi 68392627 ref XM 686039.1	PREDICTED: Danio rerio hypotheti...	123	1e-24
gi 28144669 emb AL928820.8	Zebrafish DNA sequence from clone...	123	1e-24
gi 44890591 gb BC066971.1	Homo sapiens chromosome 18 open re...	115	2e-22
gi 53133395 emb AJ720368.1	Gallus gallus mRNA for hypothetical	97.6	6e-17
gi 71896400 ref NM 001031013.1	Gallus gallus similar to Protein	97.6	6e-17
gi 32398638 emb AL837520.26	Mouse DNA sequence from clone RP...	85.7	2e-13
gi 49900684 gb BC076211.1	Danio rerio zgc:92731, mRNA (cDNA ...	71.9	3e-09
gi 50540225 ref NM 001002580.1	Danio rerio zgc:92731 (zgc:92731	71.9	3e-09
gi 12860744 dbj AK020227.1	Mus musculus 15 days embryo embry...	56.0	2e-04
gi 61696641 gb AY803104.1	Sus scrofa chromosome 17 clone pkmCon	48.1	0.047
gi 58382298 ref XM 311847.2	Anopheles gambiae str. PEST ENSA...	48.1	0.047
gi 57968359 ref XM 563067.1	Anopheles gambiae str. PEST ENSA...	48.1	0.047
gi 77020632 gb AC155164.5	Mus musculus BAC clone RP24-74L7 f...	42.1	2.9
gi 44844522 emb BX088564.10	Zebrafish DNA sequence from clon...	42.1	2.9
gi 25046376 gb AC087063.20	Mus musculus strain C57BL/6J clon...	42.1	2.9
gi 86279771 gb CP000133.1	Rhizobium etli CFN 42, complete genom	42.1	2.9
gi 15873053 emb AJ328635.1 HSA328635	Homo sapiens genomic seq...	42.1	2.9
gi 3337310 gb AC005284.1 AC005284	Homo sapiens chromosome 17,...	42.1	2.9

## Alignments

Get selected sequences

Select all

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> ☐ gi|40317614|ref|NM 020182.3| **U E G** Homo sapiens transmembrane, prostate androger transcript variant 1, mRNA  
Length=4930

Score = 1322 bits (667), Expect = 0.0  
Identities = 688/688 (100%), Gaps = 0/688 (0%)  
Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	567	.....	626
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	627	.....	686
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCCGCTCGGCCACCGACCG	353

Sbjct	687	.....	746
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	747	.....	806
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	807	.....	866
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	867	.....	926
Query	534	GAACCGGGAGTCGGTGCGCGACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	927	.....	986
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	987	.....	1046
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	1047	.....	1106
Query	714	CTACCCGGGGTCTCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	1107	.....	1166
Query	774	GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	1167	.....	1226
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	1227	.....	1254

Score = 188 bits (95), Expect = 2e-44  
 Identities = 95/95 (100%), Gaps = 0/95 (0%)  
 Strand=Plus/Plus

Query	47	GGCAGCCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA	106
Sbjct	440	.....	499
Query	107	TCACGGAGCTGGAGTTTGTTTCAGATCATCATCATC	141
Sbjct	500	.....	534

Score = 56.0 bits (28), Expect = 2e-04  
 Identities = 28/28 (100%), Gaps = 0/28 (0%)  
 Strand=Plus/Plus

Query	1	ATGCACCGCTTGATGGGGGTCAACAGCA	28
Sbjct	394	.....	421

> [gi|40317615|ref|NM\\_199169.1|](#) **UIG** Homo sapiens transmembrane, prostate androgen : transcript variant 2, mRNA  
 Length=4538

Score = 1322 bits (667), Expect = 0.0  
 Identities = 688/688 (100%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	175	.....	234
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCTCAGAAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	235	.....	294
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCCACCGACCG	353

Sbjct	295	.....	354
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	355	.....	414
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	415	.....	474
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACT	533
Sbjct	475	.....	534
Query	534	GAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	535	.....	594
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	595	.....	654
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	655	.....	714
Query	714	CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGG	773
Sbjct	715	.....	774
Query	774	GACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	775	.....	834
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	835	.....	862

Score = 63.9 bits (32), Expect = 8e-07  
 Identities = 32/32 (100%), Gaps = 0/32 (0%)  
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	111	.....	142

> [gi|40317619|ref|NM\\_199171.1|](#) **U1E G** Homo sapiens transmembrane, prostate androger transcript variant 4, mRNA  
 Length=4590

Score = 1322 bits (667), Expect = 0.0  
 Identities = 688/688 (100%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	227	.....	286
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	287	.....	346
Query	294	AGTGTCAAGCAACGGAATCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCCACCGACCG	353
Sbjct	347	.....	406
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	407	.....	466
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	467	.....	526
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACT	533
Sbjct	527	.....	586

Query	534	GAACCGGGAGTCGGTGC	CGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	587	.....	.....	646
Query	594	TAGTGCCAGGCTGGGCGG	CCCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	647	.....	.....	706
Query	654	CTACGGCAGCGGCGGGCG	CATGGAGGGGCGCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	707	.....	.....	766
Query	714	CTACCGGGGTCCTCCTTCC	CAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	767	.....	.....	826
Query	774	GACCCGGCTCCACCACACAC	ACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	827	.....	.....	886
Query	834	GAAGGATAAACAGAAAGGAC	ACCCTCTC	861
Sbjct	887	.....	.....	914

Score = 63.9 bits (32), Expect = 8e-07  
Identities = 32/32 (100%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	163	.....	194

> [gi|40317617|ref|NM\\_199170.1|](#) **U****G** Homo sapiens transmembrane, prostate androgen :  
transcript variant 3, mRNA  
Length=4531

Score = 1322 bits (667), Expect = 0.0  
Identities = 688/688 (100%), Gaps = 0/688 (0%)  
Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233	
Sbjct	168	.....	227	
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293	
Sbjct	228	.....	287	
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCTCGGCCACCGACCG	353	
Sbjct	288	.....	347	
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413	
Sbjct	348	.....	407	
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473	
Sbjct	408	.....	467	
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGA	533	
Sbjct	468	.....	527	
Query	534	GAACCGGGAGTCGGTGC	CGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	528	.....	.....	587
Query	594	TAGTGCCAGGCTGGGCGG	CCCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	588	.....	.....	647
Query	654	CTACGGCAGCGGCGGGCG	CATGGAGGGGCGCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	648	.....	.....	707
Query	714	CTACCGGGGTCCTCCTTCC	CAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	708	.....	.....	767

Query 774 GACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA 833  
Sbjct 768 ..... 827

Query 834 GAAGGATAAACAGAAAGGACACCCTCTC 861  
Sbjct 828 ..... 855

Score = 63.9 bits (32), Expect = 8e-07  
Identities = 32/32 (100%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

Query 110 CGGAGCTGGAGTTTGTTCAGATCATCATCATC 141  
Sbjct 104 ..... 135

> [gi|50492890|emb|CR612083.1|](#) **U** full-length cDNA clone CS0DJ015YF12 of T cells (Ji  
Cot 10-normalized of Homo sapiens (human)  
Length=901

Score = 1322 bits (667), Expect = 0.0  
Identities = 688/688 (100%), Gaps = 0/688 (0%)  
Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA 233  
Sbjct 6 ..... 65

Query 234 GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC 293  
Sbjct 66 ..... 125

Query 294 AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCCGCTCGGCCCACCGACCG 353  
Sbjct 126 ..... 185

Query 354 CCTGGCCGTGCCGCCCTTCGCCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC 413  
Sbjct 186 ..... 245

Query 414 GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC 473  
Sbjct 246 ..... 305

Query 474 CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCT 533  
Sbjct 306 ..... 365

Query 534 GAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA 593  
Sbjct 366 ..... 425

Query 594 TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG 653  
Sbjct 426 ..... 485

Query 654 CTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCA 713  
Sbjct 486 ..... 545

Query 714 CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG 773  
Sbjct 546 ..... 605

Query 774 GACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA 833  
Sbjct 606 ..... 665

Query 834 GAAGGATAAACAGAAAGGACACCCTCTC 861  
Sbjct 666 ..... 693

> [gi|16303741|gb|AF305616.1|AF305616](#) **U E G** Homo sapiens STAG1/PMEPA1 mRNA, complet  
Length=4839



Score = 1322 bits (667), Expect = 0.0  
Identities = 688/688 (100%), Gaps = 0/688 (0%)  
Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	494	.....	553
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCGTGTGGCCCTCGGAGAGCAC	293
Sbjct	554	.....	613
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCCGCCCTCGGCCACCGACCG	353
Sbjct	614	.....	673
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	674	.....	733
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	734	.....	793
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	794	.....	853
Query	534	GAACCGGGAGTCGGTGC GCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	854	.....	913
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	914	.....	973
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	974	.....	1033
Query	714	CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGG	773
Sbjct	1034	.....	1093
Query	774	GACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	1094	.....	1153
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	1154	.....	1181

Score = 188 bits (95), Expect = 2e-44  
Identities = 95/95 (100%), Gaps = 0/95 (0%)  
Strand=Plus/Plus

Query	47	GGCAGCCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA	106
Sbjct	367	.....	426
Query	107	TCACGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	427	.....	461

Score = 56.0 bits (28), Expect = 2e-04  
Identities = 28/28 (100%), Gaps = 0/28 (0%)  
Strand=Plus/Plus

Query	1	ATGCACCGCTTGATGGGGGTCAACAGCA	28
Sbjct	321	.....	348

>gi|22121998|gb|AY128643.1| U E G Homo sapiens PMEPA1 variant A protein mRNA, cor  
Length=1818

Score = 1322 bits (667), Expect = 0.0  
 Identities = 688/688 (100%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	168	.....	227
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	228	.....	287
Query	294	AGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCACCGACCG	353
Sbjct	288	.....	347
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCACCTATCC	413
Sbjct	348	.....	407
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	408	.....	467
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	468	.....	527
Query	534	GAACCGGGAGTCGGTGCGCGACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	528	.....	587
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	588	.....	647
Query	654	CTACGGCAGCGGGCGGGCGCATGGAGGGGCGCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	648	.....	707
Query	714	CTACCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	708	.....	767
Query	774	GACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	768	.....	827
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	828	.....	855

Score = 63.9 bits (32), Expect = 8e-07  
 Identities = 32/32 (100%), Gaps = 0/32 (0%)  
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	104	.....	135

> [gi|9255808|gb|AF224278.1|AF224278](#) **UEG** Homo sapiens PMEPA1 protein (PMEPA1) mRNA  
 Length=1141

Score = 1322 bits (667), Expect = 0.0  
 Identities = 688/688 (100%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	164	.....	223
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	224	.....	283
Query	294	AGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCACCGACCG	353
Sbjct	284	.....	343

Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	344	.....	403
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	404	.....	463
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	464	.....	523
Query	534	GAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	524	.....	583
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	584	.....	643
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	644	.....	703
Query	714	CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	704	.....	763
Query	774	GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	764	.....	823
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	824	.....	851

Score = 63.9 bits (32), Expect = 8e-07  
 Identities = 32/32 (100%), Gaps = 0/32 (0%)  
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	100	.....	131

> [gi|16198474|gb|BC015918.1|](#) **U1E G** Homo sapiens transmembrane, prostate androgen :  
 (cDNA clone IMAGE:4559576), partial cds  
 Length=1061

Score = 1314 bits (663), Expect = 0.0  
 Identities = 687/688 (99%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	154	.....	213
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	214	.....	273
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCTCGGCCCACCGACCG	353
Sbjct	274	.....	333
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	334	.....	393
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	394	.....G.....	453
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	454	.....	513
Query	534	GAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593

Sbjct	514	.....	573
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	574	.....	633
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	634	.....	693
Query	714	CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGG	773
Sbjct	694	.....	753
Query	774	GACCCGGCTCCACCACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	754	.....	813
Query	834	GAAGGATAAACAGAAAGGACACCCTCTC	861
Sbjct	814	.....	841

Score = 188 bits (95), Expect = 2e-44  
 Identities = 95/95 (100%), Gaps = 0/95 (0%)  
 Strand=Plus/Plus

Query	47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA	106
Sbjct	27	.....	86
Query	107	TCACGGAGCTGGAGTTTGTTCAGATCATCATCATC	141
Sbjct	87	.....	121

> [gi|51593770|gb|BC080635.1|](#) **UIG** Homo sapiens transmembrane, prostate androgen inc  
 variant 2, mRNA (cDNA clone MGC:99523 IMAGE:6569922),  
 complete cds  
 Length=1060

Score = 1298 bits (655), Expect = 0.0  
 Identities = 685/688 (99%), Gaps = 0/688 (0%)  
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	153	.....T.....	212
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	213	.....	272
Query	294	AGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCTCGGCCCACCGACCG	353
Sbjct	273	.....	332
Query	354	CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	333	.....	392
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	393	.....G.....G.....	452
Query	474	CCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCAGCAGCTGGAAC	533
Sbjct	453	.....	512
Query	534	GAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct	513	.....	572
Query	594	TAGTGCCAGGCTGGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG	653
Sbjct	573	.....	632
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	633	.....	692

```

Query 714 CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGG 773
Sbjct 693 ..... 752

Query 774 GACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA 833
Sbjct 753 ..... 812

Query 834 GAAGGATAAACAGAAAGGACACCCTCTC 861
Sbjct 813 ..... 840

```

Score = 63.9 bits (32), Expect = 8e-07  
 Identities = 32/32 (100%), Gaps = 0/32 (0%)  
 Strand=Plus/Plus

```

Query 110 CGGAGCTGGAGTTTGTTCAGATCATCATCATC 141
Sbjct 89 ..... 120

```

> [gi|11546043|emb|AL035541.15|HS718J7](#) **EID** Human DNA sequence from clone RP4-718J7  
 Contains the PCK1 gene for soluble phosphoenolpyruvate  
 carboxykinase 1, the ZBP1 gene for Z-DNA binding protein  
 1, the 3' end of the TMEPAI gene for transmembrane prostate  
 androgen induced mRNA, two putative novel genes, the 5' end  
 of the CTCFL gene for CCTC-binding factor (zinc finger)-like  
 and a CpG island, complete sequence  
 Length=130435

Score = 1039 bits (524), Expect = 0.0  
 Identities = 545/545 (100%), Gaps = 0/545 (0%)  
 Strand=Plus/Minus

```

Query 317 AGCCGCAGGTCTACGCCCCGCTCGGCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCC 376
Sbjct 128443 ..... 128384

Query 377 AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACC 436
Sbjct 128383 ..... 128324

Query 437 TGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCACCCCTACCAGGGCCCCCTGCA 496
Sbjct 128323 ..... 128264

Query 497 CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAGTGAACCGGGAGTCGGTGCGCGCAC 556
Sbjct 128263 ..... 128204

Query 557 CCCCAAACAGAAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCT 616
Sbjct 128203 ..... 128144

Query 617 GnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGCGCATGG 676
Sbjct 128143 ..... 128084

Query 677 AGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCTCTCTTCCAGC 736
Sbjct 128083 ..... 128024

Query 737 ACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACACACACA 796
Sbjct 128023 ..... 127964

Query 797 TCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACC 856
Sbjct 127963 ..... 127904

Query 857 CTCTC 861
Sbjct 127903 ..... 127899

```

Score = 107 bits (54), Expect = 6e-20

Identities = 54/54 (100%), Gaps = 0/54 (0%)  
Strand=Plus/Minus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAATCCCAGAG 318  
Sbjct 128929 ..... 128876

> [gi|15824468|gb|AF305426.1|AF305426](#) **D** Homo sapiens solid tumor-associated 1 prote  
gene, complete cds  
Length=61505

Score = 1039 bits (524), Expect = 0.0  
Identities = 545/545 (100%), Gaps = 0/545 (0%)  
Strand=Plus/Plus

Query 317 AGCCCGAGGTCTACGCCCCGCCTCGGCCACCGACCGCTGGCCGTGCCGCCCTTCGCCC 376  
Sbjct 57303 ..... 57362

Query 377 AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACC 436  
Sbjct 57363 ..... 57422

Query 437 TGCCACCCACCATCTCGCTGTCTAGACGGGGAGGAGCCCCACCCCTACCAGGGCCCCCTGCA 496  
Sbjct 57423 ..... 57482

Query 497 CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACGAACCGGGAGTCGGTGCGCGCAC 556  
Sbjct 57483 ..... 57542

Query 557 CCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCT 616  
Sbjct 57543 ..... 57602

Query 617 GnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGCGCATGG 676  
Sbjct 57603 ..... 57662

Query 677 AGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCTCTCTTCCAGC 736  
Sbjct 57663 ..... 57722

Query 737 ACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACACACACA 796  
Sbjct 57723 ..... 57782

Query 797 TCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACC 856  
Sbjct 57783 ..... 57842

Query 857 CTCTC 861  
Sbjct 57843 ..... 57847

Score = 182 bits (92), Expect = 1e-42  
Identities = 92/92 (100%), Gaps = 0/92 (0%)  
Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA 233  
Sbjct 50270 ..... 50329

Query 234 GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAG 265  
Sbjct 50330 ..... 50361

Score = 125 bits (63), Expect = 3e-25  
Identities = 63/63 (100%), Gaps = 0/63 (0%)  
Strand=Plus/Plus

Query 47 GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA 106  
Sbjct 367 ..... 426

Query 107 TCA 109  
Sbjct 427 ... 429

Score = 107 bits (54), Expect = 6e-20  
Identities = 54/54 (100%), Gaps = 0/54 (0%)  
Strand=Plus/Plus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAATCCCAGAG 318  
Sbjct 56817 ..... 56870

Score = 63.9 bits (32), Expect = 8e-07  
Identities = 32/32 (100%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

Query 110 CGGAGCTGGAGTTTGTTCAGATCATCATCATC 141  
Sbjct 50206 ..... 50237

Score = 56.0 bits (28), Expect = 2e-04  
Identities = 28/28 (100%), Gaps = 0/28 (0%)  
Strand=Plus/Plus

Query 1 ATGCACCGCTTGATGGGGGTCAACAGCA 28  
Sbjct 321 ..... 348

> [gi|55652999|ref|XM\\_514746.1|](#) **G** PREDICTED: Pan troglodytes LOC458363 (LOC458363),  
Length=1059

Score = 995 bits (502), Expect = 0.0  
Identities = 538/543 (99%), Gaps = 0/543 (0%)  
Strand=Plus/Plus

Query 319 CCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCTGGCCGTGCCGCCCTTCGCCCAG 378  
Sbjct 454 ..... 513

Query 379 CGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTG 438  
Sbjct 514 .....C..... 573

Query 439 CCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCACCCTACCAGGGCCCCCTGCACC 498  
Sbjct 574 ..G.....G..... 633

Query 499 CTCCAGCTTCGGGACCCCCGAGCAGCAGCTGGAAGTGAACCGGGAGTCGGTGCGCGCACCC 558  
Sbjct 634 ..... 693

Query 559 CCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCTGn 618  
Sbjct 694 ..... 753

Query 619 nnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGCGCATGGAG 678  
Sbjct 754 ..... 813

Query 679 GGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCAC 738  
Sbjct 814 .....A..... 873

Query 739 CAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACACACATC 798  
Sbjct 874 ..... 933

Query 799 GCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCCT 858  
Sbjct 934 .....C..... 993

Query 859 CTC 861  
Sbjct 994 ... 996

Score = 107 bits (54), Expect = 6e-20  
Identities = 54/54 (100%), Gaps = 0/54 (0%)  
Strand=Plus/Plus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAATCCCAGAG 318  
Sbjct 294 ..... 347

> [gi|73992626|ref|XM\\_543070.2|](#) **G** PREDICTED: Canis familiaris similar to Transmembrane  
androgen-induced protein (Solid tumor-associated 1 protein)  
(LOC485945), mRNA  
Length=2142

Score = 872 bits (440), Expect = 0.0  
Identities = 634/691 (91%), Gaps = 3/691 (0%)  
Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCTTCATCAGCCGGCACAGCCA 233  
Sbjct 471 .....G..C.....G..... 530

Query 234 GGGGCGGAGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC 293  
Sbjct 531 ...CA.....G.....C.....G.....C.....G..C..... 590

Query 294 AGTGTTCAGGCAACGGAATCCCAGAGCCGAGGTCTACGCCCCGCCTCGGCCACCGACCG 353  
Sbjct 591 G.....G....G.....T.....T..GA..... 650

Query 354 CCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC 413  
Sbjct 651 .....C.....A.....C.....C.. 710

Query 414 GTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC 473  
Sbjct 711 .....C.....G.....G..... 770

Query 474 CCCACCCTACCAGGGCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCT 533  
Sbjct 771 ...G.....G.....G.....G.. 830

Query 534 GAACCGGGAGTCGGTGCGCGACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGA 593  
Sbjct 831 .....C.....G.....G.....C..... 890

Query 594 TAGTGCCAGGCTGGGCGGCCCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTG 653  
Sbjct 891 C.....T..T..... 950

Query 654 CTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCA 713  
Sbjct 951 .....GG....T.....C..... 1010

Query 714 CTACCCGGGGTCC---TCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGA 770  
Sbjct 1011 .....CCGG.....C..... 1070



Query 771 GGGGACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAA 830  
Sbjct 1071 .....C.....G.....C.....G.....A....TGC..... 1130

Query 831 AGAGAAGGATAAAACAGAAAGGACACCCCTCTC 861  
Sbjct 1131 ...A.....C.....G..... 1161

Score = 44.1 bits (22), Expect = 0.73  
Identities = 28/30 (93%), Gaps = 0/30 (0%)  
Strand=Plus/Plus

Query 112 GAGCTGGAGTTTGTTCAGATCATCATCATC 141  
Sbjct 409 .....G.....C..... 438



> gi|82524234|emb|CR956367.12|  Pig DNA sequence from clone PigE-122C21 on chrom  
sequence  
Length=124577

Score = 644 bits (325), Expect = 0.0  
Identities = 494/544 (90%), Gaps = 3/544 (0%)  
Strand=Plus/Minus

Query	317	AGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCTGGCCGTGCCGCCCTTCGCCC	376
Sbjct	55054	.....C.....G.....G.....C.....	54995
Query	377	AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACC	436
Sbjct	54994	.....C.....C.....	54935
Query	437	TGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCA	496
Sbjct	54934	....G.....G.....C.....G..G.....G.....	54875
Query	497	CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAGTGAACCGGGAGTCGGTGCGCGCAC	556
Sbjct	54874	.G.....G.....G.....C.....G.	54815
Query	557	CCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCT	616
Sbjct	54814	....G.....C.....C..C....T.....	54755
Query	617	GnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGGCGGCATGG	676
Sbjct	54754	.T.....GG.....	54695
Query	677	AGGGGCCGCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGG---GTCCTCCTTCC	733
Sbjct	54694	....C.....C.....G.....C..CGCC...A.....	54635
Query	734	AGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACACAC	793
Sbjct	54634	.....C...C.....G....C.G...	54575
Query	794	ACATCGCGCCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGAC	853
Sbjct	54574	.....C..G..G.....A.G..GGC....G.....G..C.	54515
Query	854	ACCC	857
Sbjct	54514	....	54511

Score = 125 bits (63), Expect = 3e-25  
Identities = 63/63 (100%), Gaps = 0/63 (0%)  
Strand=Plus/Minus

Query	47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA	106
Sbjct	104963	.....	104904
Query	107	TCA	109
Sbjct	104903	...	104901

Score = 91.7 bits (46), Expect = 3e-15  
Identities = 79/90 (87%), Gaps = 0/90 (0%)  
Strand=Plus/Minus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	59532	.....C..T..C.....C..G.....	59473
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTC	263
Sbjct	59472	...CA..C....G.....C..G.....	59443

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 48/54 (88%), Gaps = 0/54 (0%)  
Strand=Plus/Minus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAATCCCAGAG 318  
 Sbjct 55548 .....C.....G.....G....GT...G..... 55495

Score = 48.1 bits (24), Expect = 0.047  
 Identities = 27/28 (96%), Gaps = 0/28 (0%)  
 Strand=Plus/Minus

Query 1 ATGCACCGCTTGATGGGGGTCAACAGCA 28  
 Sbjct 105009 .....A..... 104982

> [gi|18605637|gb|BC023092.1|](#) **U.E.G** Mus musculus cDNA clone IMAGE:3989996, partial  
 Length=1079

Score = 531 bits (268), Expect = 1e-147  
 Identities = 528/608 (86%), Gaps = 12/608 (1%)  
 Strand=Plus/Plus

Query 178 TGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGG 237  
 Sbjct 188 .....A..C.....A.....CC 247

Query 238 CGGAGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTG 297  
 Sbjct 248 A.....C....GA.....G.....C.....A.....T..G... 307

Query 298 TCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCTCGGCCCACCGACCGCCTG 357  
 Sbjct 308 .....T---.....G..G.....A.....T.....T.....A..C 364

Query 358 GCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTAC 417  
 Sbjct 365 ..T.....C.....AT.....-.....A.....A.....C..C... 415

Query 418 CTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTTCAGACGGGGAGGAGCCCCCA 477  
 Sbjct 416 .....A..T.C.....A.....T..T..... 475

Query 478 CCCTACCAGGGCCCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAAC 537  
 Sbjct 476 .....A.....T.....A.....G..... 535

Query 538 CGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGT 597  
 Sbjct 536 .....A..T.....T...C.G.....T..A..C..C 595

Query 598 GCCAGGCTGGGCGGCCCCCTGnnnnnnnnAGCAGTAACTCGGGCATCAGCGCCACGTGCTAC 657  
 Sbjct 596 A...T.....G.....T.....C..... 655

Query 658 GGCAGCGGCGGGCGCATGGAGGGGCGCCGCCACCTACAGCGAGGTCATCGGCCACTAC 717  
 Sbjct 656 A.....T.....C..... 715

Query 718 CCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCGCCCTCCTTGCTGGAGGGGACC 777  
 Sbjct 716 ..T..C.....A..T.AC.....AT.....C....A..... 775

Query 778 CGGCTCCA 785  
 Sbjct 776 ..... 783

Score = 111 bits (56), Expect = 4e-21  
 Identities = 71/76 (93%), Gaps = 0/76 (0%)  
 Strand=Plus/Plus

Query 47 GGCAGCCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGA 106  
 Sbjct 57 .....G.....C.G.....CC..... 116

Query 107 TCACGGAGCTGGAGTT 122  
 Sbjct 117 ..... 132